REMARKS/ARGUMENTS

Support for the newly added claims can be found throughout the specification and is specified below. No new matter is introduced.

Support for Independent Claim 46.

Support for independent claim 46 is generally found on pages 22-24 where the specification provides a detailed description of separating repetitive and non-repetitive DNA using hydroxyapatite. More specifically, the specification supports the preamble of claim 46 as follows:

> A method of producing a genomic library enriched for genes and regulatory sequences from a eukaryotic genome, said method comprising:

The preamble language finds support generally on page 9, lines 1-5, where the specification teaches that the general purpose of the invention is to produce genomic libraries enriched for gene and regulatory sequences by eliminating repetitive DNA, and at page 22 where it is written that one can select for unique DNA by elimination of repetitive DNA via hybridization.

> cleaving a eukaryotic genome having native methylation into fragments of double stranded DNA;

The step of cleaving into fragments finds support on page 17 where genomic DNA is cleaved using a restriction enzyme and on pages 24, 30 and 34 where DNA fragmentation by mechanical means is described;

> denaturing the double stranded DNA fragments;
>
> selectively hybridizing the fragments at Cot values of between approximately 0.01 and 100 to yield a population of double-stranded, repetitive DNA fragments and a single-stranded population of non-repetitive fragments enriched for genes;

The steps of denaturing and selectively hybridizing fragments of DNA find support on pages 22-23 of the specification with specific Cot values found in original claim 5.

> separating the two populations by hydroxyapatite chromatography;
>
> selecting the non-repetitive population enriched for genes; and,

The steps of separating and selecting single stranded fragments of DNA find support on page 22, last two sentences.

> inserting the non-repetitive population of fragments into a vector to produce a genomic library enriched for genes from a eukaryotic genome.

The inserting of the non-repetitive gene enriched sequences containing fragments into a vector is generally described in original claim 1, and more specifically on page 22, last sentence, describing M13 as a vector.

The dependent claims find support as follows:

Claim 47 reciting sequencing finds support on page 12 at the third full paragraph.

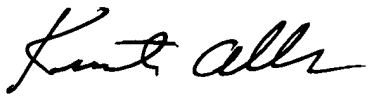
Claim 48 finds support at original claim 2.

Claim 49 reciting methylation insensitive restriction enzymes finds support on page 11, line 14.

Claims 50-57 find support in originally presented claims 22, 34, 8, 9, 10, 12, 11, 13, respectively.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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